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<223> CAB1 heavy chain

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Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
        35                  40                  45
Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
    50                  55                  60
Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65                  70                  75                  80
Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys
            85                  90                  95
Asn Glu Gly Thr Pro Thr Gly Pro Tyr Tyr Phe Asp Tyr Trp Gly Gln
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Gly Thr Thr Val Thr Val Ser Ser
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<220>
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<400> 3

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<213> Artificial Sequence

<220>
<223> CAB1 light chain

<400> 4

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            20                  25                  30
His Trp Phe Gln Gln Lys Pro Gly Thr Ser Pro Lys Leu Trp Ile Tyr
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3

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Ser Thr Ser Asn Leu Ala Ser Gly Val Pro Ala Arg Phe Ser Gly Ser
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Gly Ser Gly Thr Ser Tyr Ser Leu Thr Ile Ser Arg Met Glu Ala Glu
65                    70                    75                    80
Asp Ala Ala Thr Tyr Tyr Cys Gln Gln Arg Ser Ser Tyr Pro Leu Thr
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Phe Gly Ala Gly Thr Lys Leu Glu Leu Lys Arg Ala Ala Thr
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<212>  PRT
<213>  Artificial Sequence

<220>
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<400>  5

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Tyr Gln Gly Lys Pro His Tyr Tyr Thr Phe Gly Lys Ala Asp Ile Ala
              35                    40                    45
Ala Asn Lys Pro Val Thr Pro Gln Thr Leu Phe Glu Leu Gly Ser Ile
    50                    55                    60
Ser Lys Thr Phe Thr Gly Val Leu Gly Gly Asp Ala Ile Ala Arg Gly
65                    70                    75                    80
Glu Ile Ser Leu Asp Asp Ala Val Thr Arg Tyr Trp Pro Gln Leu Thr
                  85                    90                    95
Gly Lys Gln Trp Gln Gly Ile Arg Met Leu Asp Leu Ala Thr Tyr Thr
              100                   105                   110
Ala Gly Gly Leu Pro Leu Gln Val Pro Asp Glu Val Thr Asp Asn Ala
              115                   120                   125
Ser Leu Leu Arg Phe Tyr Gln Asn Trp Gln Pro Gln Trp Lys Pro Gly
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Ala Val Lys Pro Ser Gly Met Pro Tyr Glu Gln Ala Met Thr Thr Arg
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Val Leu Lys Pro Leu Lys Leu Asp His Thr Trp Ile Asn Val Pro Lys
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Ala Glu Glu Ala His Tyr Ala Trp Gly Tyr Arg Asp Gly Lys Ala Val
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Arg Val Ser Pro Gly Met Leu Asp Ala Gln Ala Tyr Gly Val Lys Thr
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225                   230                   235                   240
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Arg Tyr Trp Arg Ile Gly Ser Met Tyr Gln Gly Leu Gly Trp Glu Met
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Asn Val Ala Leu Ala Pro Leu Pro Val Ala Glu Val Asn Pro Pro Ala
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Phe Gly Ser Tyr Val Ala Phe Ile Pro Glu Lys Gln Ile Gly Ile Val
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Met Leu Ala Asn Thr Ser Tyr Pro Asn Pro Ala Arg Val Glu Ala Ala
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Tyr His Ile Leu Glu Ala Leu Gln
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<212>   PRT
<213>   Artificial Sequence
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<220>
<223> consensus mutation

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Tyr Met His Trp Leu Arg Gln Gly Pro Glu Gln Gly Leu Glu Trp Ile
        35   40   45
Gly Trp Ile Asp Pro Glu Asn Gly Asp Thr Glu Tyr Ala Pro Lys Phe
    50   55   60
Gln Gly Lys Ala Thr Phe Thr Thr Asp Thr Ser Ser Asn Thr Ala Tyr
65   70   75   80

<210> 8
<211> 80
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus mutation

<400> 8

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                20   25   30
Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Gly Ser Gly Gly Gly
        35   40   45
Gly Ser Gly Gly Gly Gly Ser Glu Asn Val Leu Thr Gln Ser Pro Ala
    50   55   60
Ile Met Ser Ala Ser Pro Gly Glu Lys Val Thr Ile Thr Cys Ser Ala
65   70   75   80

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<211> 84
<212> PRT
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<220>
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Ser Ser Ser Val Ser Tyr Met His Trp Phe Gln Gln Lys Pro Gly Thr
1   5   10   15
Ser Pro Lys Leu Trp Ile Tyr Ser Thr Ser Asn Leu Ala Ser Gly Val
                20   25   30
Pro Ala Arg Phe Ser Gly Ser Gly Ser Gly Thr Ser Tyr Ser Leu Thr
        35   40   45
Ile Ser Arg Met Glu Ala Glu Asp Ala Ala Thr Tyr Tyr Cys Gln Gln

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     50                      55                  60
Arg Ser Ser Tyr Pro Leu Thr Phe Gly Ala Gly Thr Lys Leu Glu Leu
65                      70                  75                  80
Lys Arg Ala Ala
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<210> 10
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<220>
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ggattaacgt gccgaaatcg gaagaggcgc attac   35

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<220>
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gctatcgtga cggtaaaccg gtgcgcgttt cgccg   35

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<210>   18
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<210>  23
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<210>    43
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gaaaaacagc tggcggagat cgtcgcgaat acgattacc                          39


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<400>  47
acgtgcagga tatggcgcgc tgggtcatgg ccaaca                             36


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taagttacat gcactggtac cagcagaagc caggcac                          37


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<400>  79
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<210>  81
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acccactcac gttcggtggc ggcaccaagc tggagct   37

FIGURE 10.

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Translation of CAB1   (1)   QVKLQQSGAELVRSGTSVKLSCTASGFNIKDSYMHWLRQGPEQGLEWIGWIDPENGDTEYAPKFQGKATFTDTSSNTAY (SEQ ID NO:7)
      human consensus (1)   Q              KP G         TES         V A G              RF I R         K

                        81                                                                   160
Translation of CAB1  (81)   LQLSSLTSEDTAVYYCNEGTPTGPYYFDYWGQGTTVTVSSGGGGSGGGGSGGGGSENVLTQSPAIMSASPGEKVTITCSA (SEQ ID NO:8)
      human consensus (81)                AR                                         QS  P S V          QT

                        161                                                                  240
Translation of CAB1 (161)   SSSVSYMHWFQQKPGTSPKLWIYSTSNLASGVPARFSGSGSGTSYSLTISRMEAEDAATYCQQRSSYPLTFGAGTKLELKRAA (SEQ ID NO:9)
      human consensus (161)         Y         V         D   K  A   L   E D               G
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